Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Period: \_\_\_\_\_\_

**Fruit Fly Genetics: Virtual Lab**

Ms. Ottolini, AP Biology

**Overview:** One of the most popular organisms for genetic studies is the fruit fly *Drosophila melanogaster.* Two traits that make *Drosophila* an excellent model organism are its rapid reproduction rate and easily distinguishable phenotypes. In our virtual lab, we will be studying the inheritance pattern of eye color in fruit flies. The "wild type" or normal fruit fly has red eyes (dominant). A recessive mutation can result in fruit flies with sepia eyes (brownish-red in juveniles and black in adults).

In this lab, we will be performing crosses between fruit flies with different eye colors to determine observed offspring phenotype ratios. We will then compare these observed ratios with expected ratios from Punnett square analyses we performed before the lab. Our tool for statistical comparison will be a chi-square analysis.

In this lab, we will be performing the cross listed in the chart below. For each cross, we will obtain our F1 offspring and re-cross them to obtain our F2 offspring:

|  |  |  |  |
| --- | --- | --- | --- |
| **Cross #** | **Type of Cross** | **Male Fly** | **Female Fly** |
| 1 | Normal Monohybrid | Sepia Eyes (Recessive) | Red Eyes (Wild Type / Dominant) |

**Pre-Lab:** Complete each of the crosses using the Punnett Squares given below.

1. Sepia-Eyed Male x Red-Eyed Female

P cross (ss x SS) F1 Cross (\_\_\_\_\_\_\_\_ x \_\_\_\_\_\_\_\_)

|  |  |
| --- | --- |
|  |  |
|  |  |

|  |  |
| --- | --- |
|  |  |
|  |  |

F1 Genotypes: F2 Genotypes:

F1 Phenotypes: F2 Phenotypes:

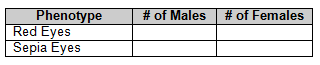
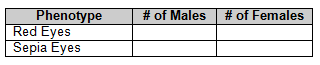
**Lab Instructions**

1. Sign in to your computer using Username: student, Password: student. Check the “Workstation Only” box.
2. Go to the following URL address: <http://www.sciencecourseware.org/vcise/drosophila/>
3. Click the “Enter as a Guest” option.
4. The first thing you must do is order the fruit flies for your first cross. Click on the computer and use the “Order Flies” icon.
5. After ordering your flies, the software will give you instructions on how to cross the flies and sort the F1 offspring by phenotype using a microscope view. Make sure you record the data for your F1 generation in your data table.
6. After you have recorded the data, you will need to establish a cross between members of your F1 generation. To do this, click on the piles of sorted flies to zoom in. Then click the “Use in New Mating” button. Do this for both a male and a female. Then return to your lab. Click on the mating jar and continue with the cross to obtain your F2 generation. Make sure you record the data for your F2 generation in your data table

**Lab Data**

***Table 1:*** Sepia-Eyed Male x Red-Eyed Female (Cross 1)

Phenotypes of the F1 Generation Phenotypes of F2 Generation

***Conclusions:*** After “eyeballing” the data, do your observed results seem to match with your expected results? Does it seem that this is an autosomal recessive method of inheritance? Why?

**Post-Lab:** Chi square analysis of F2 offspring.

In this section, we will determine whether to accept or reject the **null hypothesis**, which states that there is no statistically significant difference between the observed (online) and expected (Punnett square) results in the F2 generation.

1. How many total offspring (males + females) were in the F2 generation from our first cross?
2. Calculate your expected #’s of flies with each phenotype using the following formula: % expected x total #.

|  |  |  |
| --- | --- | --- |
| **Phenotype** | **% Expected**  **(expressed as a decimal)** | **# of flies expected:**  **% expected x total # of flies** |
| Red Eyes |  |  |
| Sepia Eyes |  |  |

Use the table below to determine your X2 value for your data.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Phenotype** | **# Observed (o)** | **# Expected (e)** | **(o-e)** | **(o-e)2** | **(o-e)2 / e** |
| Red Eyes |  |  |  |  |  |
| Sepia Eyes |  |  |  |  |  |

Total (add the values in the last column) = **X2 value** = \_\_\_\_\_\_\_\_\_

1. How many degrees of freedom should we use? Remember, the degrees of freedom represent the number of classes of data / independent variables (eye colors) minus one.

**Degrees of Freedom =** \_\_\_\_\_\_\_\_\_

1. Use the chart below to determine the critical value at a probability value of p = 0.05 and the degrees of freedom value you calculated in #3.

**Critical Value =** \_\_\_\_\_\_\_\_\_

1. Based on your critical value, do you accept or reject your null hypothesis?

If the X2 value that you calculated is higher than the critical value, then you can reject the null hypothesis.

If the X2 value is lower than the critical value, then you can accept the null hypothesis.